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Nota di contenuto	Protein Structure Comparison: Algorithms and Applications -- Spatial Pattern Detection in Structural Bionformatics -- Geometric Methods for Protein Structure Comparison -- Identifying Flat Regions and Slabs in Protein Structures -- OPTIMA: A New Score Function for the Detection of Remote Homologs -- A Comparison of Methods for Assessing the Structural Similarity of Proteins -- Prediction of Protein Secondary Structure at High Accuracy Using a Combination of Many Neural Networks -- Self-consistent Knowledge-Based Approach to Protein Design -- Protein Structure from Solid-State NMR -- Learning Effective

The papers collected in this volume reproduce contributions by leading scholars to an international school and workshop which was organized and held with the goal of taking a snapshot of a discipline undergoing rapid growth. Indeed, the area of protein folding, docking and alignment is developing in response to needs for a mix of heterogeneous expertise spanning biology, chemistry, mathematics, computer science, and statistics, among others. Some of the problems encountered in this area are not only important for the scientific challenges they pose, but also for the opportunities they disclose in terms of medical and industrial exploitation. A typical example is offered by protein-drug interaction (docking), a problem posing daunting computational problems at the crossroads of geometry, physics and chemistry, and, at the same time, a problem with unimaginable implications for the pharmacopoeia of the future. The school focused on problems posed by the study of the mechanisms of protein folding, and explored different ways of attacking these problems under objective evaluations of the methods. Together with a relatively small core of consolidated knowledge and tools, important reflections were brought to this effort by studies in a multitude of directions and approaches. It is obviously impossible to predict which, if any, among these techniques will prove completely successful, but it is precisely the implicit dialectic among them that best conveys the current flavor of the field. Such unique diversity and richness inspired the format of the meeting, and also explains the slight departure of the present volume from the typical format in this series: the exposition of the current state of the field is complemented here by a selection of qualified specialized contributions.